Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1 to 27 (canceled)

Claim 28 (Currently Amended)

An isolated nucleic acid ~~having~~ consisting of a nucleotide sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 29 (Currently Amended)

An isolated nucleic acid ~~having~~ consisting of a nucleotide sequence selected from the group consisting of SEQ ID No: 1 and the complement of SEQ ID No: 1.

Claim 30 (Currently Amended)

An isolated nucleic acid ~~having~~ consisting of a nucleotide sequence selected from the group consisting of SEQ ID No: 2 and the complement of SEQ ID No: 2.

Claim 31 (Previously Presented)

A cloning or expression vector containing a nucleic acid sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 32 (Previously Presented)

A vector of claim 31 which is a plasmid selected from the group consisting of pRegX3Bc1 and pRegX3Mt1 deposited at CNCM under Nos. I-1765 and I-1766, respectively.

Claim 33 (Canceled)

Claim 34 (Currently Amended)

A nucleotide probe ~~or nucleotide primer comprising~~ consisting of 24 consecutive nucleotides selected from a sequence selected from the group consisting of SEQ ID No:1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 35 (Currently Amended)

A nucleotide probe ~~comprising a~~ consisting of a nucleotide sequence selected from the group consisting of sequence SEQ ID

No: 1, the complement of SEQ ID No: 1, their corresponding RNA sequences and their corresponding ~~gene[s]~~ gene(s).

Claim 36 (Currently Amended)

A nucleotide probe having a sequence comprising two successive sequences according to SEQ ID No: 1 followed by a sequence according to SEQ ID No: 2.

Claim 37 (Currently Amended)

A nucleotide probe ~~that consists~~ consisting of 21 ~~base pairs~~ consecutive nucleotides ~~having a sequence~~ of a region of sequence SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or the complement of said region.

Claim 38 (Currently Amended)

A nucleotide probe consisting of a nucleotide ~~comprising a~~ sequence which consists ~~composed~~ of nucleotides in positions 31 to 51 of SEQ ID No: 2 or the complement of said sequence.

Claim 39 (Canceled)

Claim 40 (Currently Amended)

A nucleotide probe ~~comprising~~ consisting of the sequence of SEQ ID No: 2 or the complement of SEQ ID No: 2.

Claim 41 (Currently Amended)

A nucleotide probe consisting of a nucleotide sequence ~~comprising one of the sequences~~ selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, the complement of SEQ ID No: 2, their corresponding RNA sequences and their corresponding ~~gene[s]~~ gene(s), wherein said nucleotide probe is labeled by digoxygenin.

Claim 42 (Canceled)

Claim 43 (Canceled)

Claim 44 (Previously Presented)

A nucleotide primer pair comprising a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5).

Claims 45 and 46 (canceled)

Claim 47 (Currently Amended)

A method of detecting a mycobacteria strain of M. tuberculosis complex in a biological sample comprising the steps of:

(1) contacting the biological sample to a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) under conditions to effect hybridization of the primers to a nucleotide sequence of mycobacteria strains of M. tuberculosis complex;

(2) amplifying said nucleotide sequence with said primers ~~effecting amplification of said nucleotide sequence nucleic acids~~;

(3) contacting ~~the biological sample containing~~ said nucleotide sequences amplified from step (2) with a nucleotide probe consisting of a nucleotide sequence selected from the group consisting ~~that comprises a sequence~~ of SEQ ID No: 1, ~~or sequence~~ SEQ ID No: 2, ~~or~~ the complement of SEQ ID No: 1, ~~or~~ the complement of SEQ ID No: 2, ~~or one of~~ their corresponding RNA sequences ~~or one of~~ and their corresponding ~~gene[s]~~ gene(s), or with a nucleotide probe having,

a sequence ~~of~~ comprising two successive ~~sequence~~ sequences of SEQ ID No: 1 followed by a sequence of SEQ ID No: 2, under conditions for formation of hybridization complexes between said probe and said nucleotide sequences amplified from step (2); and

(4) detecting the presence or absence of ~~if any hybridization~~ complexes, wherein the presence of ~~are present, which~~ complexes ~~indicate~~ is indicative of a presence of a mycobacteria strain of *M. tuberculosis* complex.

Claim 48 (Canceled)

Claim 49 (Currently Amended)

The method of claim 47 wherein the sequence of the nucleotide probe ~~comprises a sequence composed~~ consists of nucleotides in positions 31 to 51 of SEQ ID No: 2 or the complement of ~~said sequence~~ SEQ ID No: 2.

Claim 50 (cancelled)

Claim 51 (cancelled)

Claim 52 (Currently Amended)

A method of identifying groups of mycobacteria belonging to a M. tuberculosis complex comprising the steps of:

(1) contacting a DNA of previously extracted strains of the M. tuberculosis complex with a nucleotide primer pair comprising a pair of primers

5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and

5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) ~~under conditions permitting a hybridization of the primers respectively 56 base pairs upstream and 62 base pairs downstream of a sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No:~~

~~2, the complement of SEQ ID No: 1 and the complement of SEQ ID No: 2,~~ to obtain amplification products; and

(2) measuring a length of the amplification products obtained from step (1), wherein said length of the amplification products enables determining the group to which said strains of M. tuberculosis complex belong.

Claim 53 (Canceled)

Claim 54 (Previously Presented)

A kit for in vitro identification of strains of mycobacteria of a M. tuberculosis complex in a biological sample comprising a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5).

Claim 55 (Currently Amended)

A method of detection and of differential diagnosis of BCG and the members of M. tuberculosis complex in a biological sample comprising the steps of:

(1) contacting the biological sample to a nucleotide primer pair comprising a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) ~~for amplification of a nucleotide sequence of mycobacteria of M. tuberculosis complex,~~ under conditions to effect hybridization

of the primers to said nucleotide sequence of mycobacteria ~~strains~~ of M. tuberculosis complex;

(2) amplifying said nucleotide sequence with said primers ~~effecting amplification of said nucleotide sequence~~;

(3) contacting the biological sample containing said nucleotide sequence amplified from step (2) with a nucleotide probe ~~of~~ having a sequence comprising two successive sequences of SEQ ID No: 1, followed by a sequence SEQ ID No: 2 under conditions for formation of hybridization complexes between said probe and said nucleotide sequences amplified from step (2);

(4) detecting any first hybridization complexes present; and

(5) determining if said first hybridization complexes are also capable of forming second hybridization complexes with a nucleotide probe, ~~comprising a~~ the sequence of which consists ~~composed~~ of nucleotides in positions 31 to 51 of SEQ ID No:2, or the complement of said sequence, for detection of sequences of nucleic acids of M. tuberculosis complex other than BCG, a presence of said second hybridization complexes being indicative of a presence of a M. tuberculosis strain different from BCG and a presence of said first hybridization complexes uniquely being indicative of the BCG.

Claim 56 (New)

The method of claim 55, wherein the biological sample is from an immunodeficient human.

Claim 57 (New)

The method of claim 56, wherein the human is infected with HIV.